

We claim:

1. A peptide fragment having the general sequence

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His-X¹-His-X²-X³-X⁴-Cys-X⁵-X⁶-Cys,

where the variables X¹ to X⁶ in the sequence have the following meanings:

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X¹ = an amino acid selected from the group of Ala, Val, Phe, Ser, Met, Trp, Tyr, Asn, Asp or Lys and the variables X² to X⁶ an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

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X² = an amino acid selected from the group of Val, Ile, Phe, Pro, Trp, Tyr, Gln, Glu or Arg and the variables X¹, X³ to X⁶ an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

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X³ = an amino acid selected from the group of Gly, Ile, Thr, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His and the variables X¹, X², X⁴ to X⁶ an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

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X⁴ = an amino acid selected from the group of Val, Phe, Pro, Cys, Met, Trp, Asn, Glu, Arg or His and the variables X¹ to X³, X⁵, X⁶ an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

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X⁵ = an amino acid selected from the group of Gly, Ser, Cys, Met, Trp, Asn, Glu, Lys or Arg and the variables X¹ to X⁴, X⁶ an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

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X⁶ = an amino acid selected from the group of Phe, Pro, Ser, Cys, Trp, Tyr or Gln and the variables X¹ to X⁵ an amino acid selected from the group of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His and

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where at least one of the variables X^1 to X^6 in the sequence is, independently of one another, Gln or Asn.

2. A peptide fragment as claimed in claim 1, in which the
5 variables X^1 to X^6 have the meanings stated in claim 1, where
at least one of the variables X^1 to X^6 in the sequence is,
independently of one another, Lys or Arg.
3. A peptide fragment as claimed in claim 1 ~~or 2~~, in which the
10 variables X^1 to X^6 in the sequence have the following meanings
independently of one another:

X^1 = an amino acid selected from the group of Ala, Val, Phe,
Ser, Met, Trp, Tyr, Asn, Asp or Lys;

15 X^2 = an amino acid selected from the group of Val, Ile, Phe,
Pro, Trp, Tyr, Gln, Glu or Arg;

20 X^3 = an amino acid selected from the group of Gly, Ile, Thr,
Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg or His;

X^4 = an amino acid selected from the group of Val, Phe, Pro,
Cys, Met, Trp, Asn, Glu, Arg or His;

25 X^5 = an amino acid selected from the group of Gly, Ser, Cys,
Met, Trp, Asn, Glu, Lys or Arg;

30 X^6 = an amino acid selected from the group of Phe, Pro, Ser,
Cys, Trp, Tyr or Gln.

claim 1

4. A peptide fragment as claimed in ~~any of claims 1 to 3~~, in
which the variables X^1 to X^6 in the sequence have the
following meanings independently of one another:

35 X^1 = an amino acid selected from the group of Phe, Ser, Asn,
Asp or Lys;

40 X^2 = an amino acid selected from the group of Val, Ile, Phe,
Pro, Gln, Glu or Arg;

X^3 = an amino acid selected from the group of Gly, Ile, Thr,
Met, Trp, Tyr, Asn, Asp, Glu, Arg or His;

45 X^4 = an amino acid selected from the group of Val, Phe, Cys,
Met, Trp, Asn, Arg or His;

X⁵ = an amino acid selected from the group of Gly, Ser, Cys, Met, Asn, Glu, Lys or Arg;

5 X⁶ = an amino acid selected from the group of Phe, Ser, Cys, or Tyr.

5. A peptide fragment as claimed in any of claims 1 to 4, in which the variables X¹ to X⁶ in the sequence have the following meanings independently of one another:

10 X¹ = Asn;

X² = Gln, Glu or Arg;

15 X³ = Gly, Thr or Tyr;

X⁴ = Asn or Arg;

X⁵ = Gly or Lys;

20 X⁶ = Cys.

6. A peptide fragment having the sequence

25 His-Gln-His-Glu-Gly-Arg-Cys-Lys-Glu-Cys

His-Asn-His-Arg-Tyr-Gly-Cys-Gly-Cys-Cys

His-Arg-His-Gly-Thr-Asn-Cys-Leu-Lys-Cys

30 His-Ile-His-Gln-Ser-Asn-Cys-Gln-Val-Cys.

7. A fusion protein comprising a protein fragment as claimed in any of claims 1 to 6. *Claim 1*

35 8. A nucleic acid fragment coding for a protein fragment as claimed in any of claims 1 to 6. *Claim 1*

40 9. A nucleic acid comprising a nucleic acid fragment as claimed in claim 8.

10. A nucleic acid coding for a fusion protein as claimed in claim 7.

45 11. A vector comprising a nucleic acid fragment as claimed in claim 8 or 10.

12. A process for preparing fusion proteins as claimed in claim 7, which comprises fusing a nucleic acid fragment as claimed in claim 8 to a gene which codes for a protein.

5 13. A process for purifying fusion proteins as claimed in claim 7, which comprises

- 10 a) bringing liquids which contain the fusion protein into contact with immobilized metal ions in such a way that an affinity linkage can form between the metal ions and the fusion protein,
- 15 b) removing unbound substances present in the liquid,
- 20 c) eluting the bound fusion protein in which [sic] the affinity linkage is abolished by changing the liquid medium and
- d) collecting the purified fusion protein.

20 *Claim 1*
14. The use of a protein fragment as claimed in any of claims 1 to 6 or of a nucleic acid fragment as claimed in claim 8 for purifying proteins.

25 15. A process for preparing protein fragments able to enter into a reversible affinity linkage with immobilized metal ions, which comprises carrying out the following steps:

- 30 a) preparing a nucleic acid library starting from any suitable nucleic acid sequence which codes for a protein fragment of the sequence

His-X¹-His-X²-X³-X⁴-Cys-X⁵-X⁶-Cys,

35 where the histidine and cysteine residues of the sequence are conserved in the nucleic acid library,

- 40 b) fusing the nucleic acids of the library to a reporter gene which makes it possible to detect the fusion protein encoded by the resulting nucleic acid via its binding to the immobilized metal ions and
- 45 c) selecting the nucleic acid sequences which display a reversible binding to the immobilized metal ions which is at least 1.5 times stronger than the sequence in the natural Helicobacter pilori [sic] ATPase-439.

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16. A process as claimed in claim 15, wherein the egf protein from *Aequoria victoria* is used as reporter gene.
- 5 17. A method for detecting proteins, which comprises detecting individual proteins which comprise a protein fragment as claimed in claim 1 in a protein mixture via antibodies which are directed against the protein fragment.
- 10 18. The use of a protein fragment as claimed in ~~any of claims 1 to 6 or of a nucleic acid fragment as claimed in claim 8~~ for purifying proteins.

Claim 1

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